



10	20	30	40	50	60	70
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	CAGTACAATC	TGCTCTGATG	CCGCATAGTT
80	90	100	110	120	130	140
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AAGCCAGTAT	CTGCTCCCTG	CTTGTGTGTT	GGAGGTCGCT	GAGTAGTGCG	CGAGCAAAAT	TTAAGCTACA
150	160	170	180	190	200	210
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ACAAGGCAAG	GCTTGACCGA	CAATTGCATG	AAGAATCTGC	TTAGGGTTAG	GCGTTTTGCG	CTGCTTCGCG
220	230	240	250	260	270	280
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATGTACGGGC	CAGATATACG	CGTTGACATT	GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC
290	300	310	320	330	340	350
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATTAGTTCAT	AGCCCATATA	TGGAGTTCGG	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG
360	370	380	390	400	410	420
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CCCAACGACC	CCCGCCCAT	GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA	GGGACTTTCC
430	440	450	460	470	480	490
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATTGACGTCA	ATGGGTGGAC	TATTTACGGT	AAACTGCCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC
500	510	520	530	540	550	560
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AAGTACGCCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	CATGACCTTA
570	580	590	600	610	620	630
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC	CATGGTGATG	CGGTTTTGGC
640	650	660	670	680	690	700
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AGTACATCAA	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG	ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA
710	720	730	740	750	760	770
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
TGGGAGTTTG	TTTTGGCACC	AAAATCAACG	GGACTTTCCA	AAATGTCGTA	ACAACTCCGC	CCCATTGACG
780	790	800	810	820	830	840
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CAAATGGGCG	GTAGGCGTGT	ACGGTGGGAG	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA
850	860	870	880	890	900	910
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CTGCTTAACT	GGCTTATCGA	AATTAATACG	ACTCACTATA	GGGAGACCCA	AGCTTCGCAG	AATTCCTGCG
920	930	940	950	960	970	980
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
GCTGCTACAG	TGTGTCCAGC	GTCCTGCCTG	GCTGTGCTGA	GCGCTGGAAC	AGTGGCGCAT	CATTCAAGTG
990	1000	1010	1020	1030	1040	1050
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CACAGTTACC	CATCCTGAGT	CTGGCACCTT	AACTGGCACA	ATTGCCAAAG	TCACAGGTGA	GCTCAGATGC
1060	1070	1080	1090	1100	1110	1120
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATACCAGGAC	ATTGTATGAC	GTTCCCTGCT	CACATGCCTG	CTTTCTTCCT	ATAATACAGA	TGCTCAACTA
1130	1140	1150	1160	1170	1180	1190
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ACTGCTCATG	TCCTTATATC	ACAGAGGGAA	ATTGGAGCTA	TCTGAGGAAC	TGCCCAGAAG	GGAAGGGCAG

FIG. 1-2

1200	1210	1220	1230	1240	1250	1260
* *	* *	* *	* *	* *	* *	* *
AGGGGTCTTG	CTCTCCTTGT	CTGAGCCATA	ACTCTTCTTT	CTACCTTCCA	GTGAACACCT	TCCCACCCCA
1270	1280	1290	1300	1310	1320	1330
* *	* *	* *	* *	* *	* *	* *
GGTCCACCTG	CTACCGCCGC	CGTCGGAGGA	GCTGGCCCTG	AATGAGCTCT	TGTCCTTGAC	ATGCCTGGTG
1340	1350	1360	1370	1380	1390	1400
* *	* *	* *	* *	* *	* *	* *
CGAGCTTTCA	ACCTAAAGA	AGTGCTGGTG	CGATGGCTGC	ATGGAAATGA	GGAGCTGTCC	CCAGAAAGCT
1410	1420	1430	1440	1450	1460	1470
* *	* *	* *	* *	* *	* *	* *
ACCTAGTGTT	TGAGCCCCTA	AAGGAGCCAG	GCGAGGGAGC	CACCACCTAC	CTGGTGACAA	GCGTGTTCGC
1480	1490	1500	1510	1520	1530	1540
* *	* *	* *	* *	* *	* *	* *
TGTATCAGCT	GAAAGCTTGA	TATCGAATTC	CGGAGGCGGA	ACCGGCAGTG	CAGCCCGAAG	CCCCGCAGTC
1550	1560	1570	1580	1590		
* *	* *	* *	* *	* *		
CCCGAGCAGC	CGTGGCC	ATG CGT CCC CTG CGC CCC CGC GCC GCG CTG CTG GCG CTC CTG				
		Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu				
1600	1610	1620	1630	1640	1650	
* *	* *	* *	* *	* *	* *	
GCC TCG CTC CTG GCC GCG CCC CCG GTG GCC CCG GCC GAG GCC CCG CAC CTG GTG CAT						
Ala Ser Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His						
1660	1670	1680	1690	1700	1710	
* *	* *	* *	* *	* *	* *	
GTG GAC GCG GCC CGC GCG CTG TGG CCC CTG CGG CGC TTC TGG AGG AGC ACA GGC TTC						
Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe						
1720	1730	1740	1750	1760	1770	
* *	* *	* *	* *	* *	* *	
TGC CCC CCG CTG CCA CAC AGC CAG GCT GAC CAG TAC GTC CTC AGC TGG GAC CAG CAG						
Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln						
1780	1790	1800	1810	1820		
* *	* *	* *	* *	* *		
CTC AAC CTC GCC TAT GTG GGC GCC GTC CCT CAC CGC GGC ATC AAG CAG GTC CGG ACC						
Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr						
1830	1840	1850	1860	1870	1880	
* *	* *	* *	* *	* *	* *	
CAC TGG CTG CTG GAG CTT GTC ACC ACC AGG GGG TCC ACT GGA CGG GGC CTG AGC TAC						
His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr						
1890	1900	1910	1920	1930	1940	
* *	* *	* *	* *	* *	* *	
AAC TTC ACC CAC CTG GAC GGG TAC CTG GAC CTT CTC AGG GAG AAC CAG CTC CTC CCA						
Asn Phe Thr His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro						
1950	1960	1970	1980	1990		
* *	* *	* *	* *	* *		
GGG TTT GAG CTG ATG GGC AGC GCC TCG GGC CAC TTC ACT GAC TTT GAG GAC AAG CAG						
Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln						

FIG. 1-3

2000	2010	2020	2030	2040	2050
* * * * *					
CAG GTG TTT GAG TGG AAG GAC TTG GTC TCC AGC CTG GCC AGG AGA TAC ATC GGT AGG					
Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg					
2060	2070	2080	2090	2100	2110
* * * * *					
TAC GGA CTG GCG CAT GTT TCC AAG TGG AAC TTC GAG ACG TGG AAT GAG CCA GAC CAC					
Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His					
2120	2130	2140	2150	2160	
* * * * *					
CAC GAC TTT GAC AAC GTC TCC ATG ACC ATG CAA GGC TTC CTG AAC TAC TAC GAT GCC					
His Asp Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala					
2170	2180	2190	2200	2210	2220
* * * * *					
TGC TCG GAG GGT CTG CGC GCC GCC AGC CCC GCC CTG CGG CTG GGA GGC CCC GGC GAC					
Cys Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp					
2230	2240	2250	2260	2270	2280
* * * * *					
TCC TTC CAC ACC CCA CCG CGA TCC CCG CTG AGC TGG GGC CTC CTG CGC CAC TGC CAC					
Ser Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His					
2290	2300	2310	2320	2330	2340
* * * * *					
GAC GGT ACC AAC TTC TTC ACT GGG GAG GCG GGC GTG CGG CTG GAC TAC ATC TCC CTC					
Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu					
2350	2360	2370	2380	2390	
* * * * *					
CAC AGG AAG GGT GCG CGC AGC TCC ATC TCC ATC CTG GAG CAG GAG AAG GTC GTC GCG					
His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala					
2400	2410	2420	2430	2440	2450
* * * * *					
CAG CAG ATC CGG CAG CTC TTC CCC AAG TTC GCG GAC ACC CCC ATT TAC AAC GAC GAG					
Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu					
2460	2470	2480	2490	2500	2510
* * * * *					
GCG GAC CCG CTG GTG GGC TGG TCC CTG CCA CAG CCG TGG AGG GCG GAC GTG ACC TAC					
Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr					
2520	2530	2540	2550	2560	
* * * * *					
GCG GCC ATG GTG GTG AAG GTC ATC GCG CAG CAT CAG AAC CTG CTA CTG GCC AAC ACC					
Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr					
2570	2580	2590	2600	2610	2620
* * * * *					
ACC TCC GCC TTC CCC TAC GCG CTC CTG AGC AAC GAC AAT GCC TTC CTG AGC TAC CAC					
Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His					
2630	2640	2650	2660	2670	2680
* * * * *					
CCG CAC CCC TTC GCG CAG CGC ACG CTC ACC GCG CGC TTC CAG GTC AAC AAC ACC CGC					
Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg					

FIG. 1-4

	2690		2700		2710		2720		2730	
*	*	*	*	*	*	*	*	*	*	*
CCG	CCG	CAC	GTG	CAG	CTG	TTG	CGC	AAG	CCG	GTG
Pro	Pro	His	Val	Gln	Leu	Leu	Arg	Lys	Pro	Val
2740		2750		2760		2770		2780		2790
*	*	*	*	*	*	*	*	*	*	*
CTG	CTG	GAT	GAG	GAG	CAG	CTC	TGG	GCC	GAA	GTG
Leu	Leu	Asp	Glu	Glu	Gln	Leu	Trp	Ala	Glu	Val
2800		2810		2820		2830		2840		2850
*	*	*	*	*	*	*	*	*	*	*
AGC	AAC	CAC	ACG	GTG	GGC	GTC	CTG	GCC	AGC	GCC
Ser	Asn	His	Thr	Val	Gly	Val	Leu	Ala	Ser	Ala
2860		2870		2880		2890		2900		2910
*	*	*	*	*	*	*	*	*	*	*
GCC	TGG	CGC	GCC	GCG	GTG	CTG	ATC	TAC	GCG	AGC
Ala	Trp	Arg	Ala	Ala	Val	Leu	Ile	Tyr	Ala	Ser
2920		2930		2940		2950		2960		
*	*	*	*	*	*	*	*	*	*	*
CGC	AGC	GTC	GCG	GTG	ACC	CTG	CGG	CTG	CGC	GGG
Arg	Ser	Val	Ala	Val	Thr	Leu	Arg	Leu	Arg	Gly
2970		2980		2990		3000		3010		3020
*	*	*	*	*	*	*	*	*	*	*
TAC	GTC	ACG	CGC	TAC	CTG	GAC	AAC	GGG	CTC	TGC
Tyr	Val	Thr	Arg	Tyr	Leu	Asp	Asn	Gly	Leu	Cys
3030		3040		3050		3060		3070		3080
*	*	*	*	*	*	*	*	*	*	*
CTG	GGC	CGG	CCC	GTG	TTC	CCC	ACG	GCA	GAG	CAG
Leu	Gly	Arg	Pro	Val	Phe	Pro	Thr	Ala	Glu	Gln
3090		3100		3110		3120		3130		
*	*	*	*	*	*	*	*	*	*	*
GAC	CCG	GTG	GCC	GCG	GCG	CCC	CGC	CCC	TTA	CCC
Asp	Pro	Val	Ala	Ala	Ala	Pro	Arg	Pro	Leu	Pro
3140		3150		3160		3170		3180		3190
*	*	*	*	*	*	*	*	*	*	*
CCC	GCG	CTG	CGG	CTG	CCG	TGC	CTT	TTG	CTG	GTG
Pro	Ala	Leu	Arg	Leu	Pro	Ser	Leu	Leu	Leu	Val
3200		3210		3220		3230		3240		3250
*	*	*	*	*	*	*	*	*	*	*
CCG	CCC	GGG	CAG	GTC	ACG	CGG	CTC	CGC	GCC	CTG
Pro	Pro	Gly	Gln	Val	Thr	Arg	Leu	Arg	Ala	Leu
3260		3270		3280		3290		3300		
*	*	*	*	*	*	*	*	*	*	*
CTG	GTC	TGG	TCG	GAT	GAA	CAC	GTG	GGC	TCC	AAG
Leu	Val	Trp	Ser	Asp	Glu	His	Val	Gly	Ser	Lys
3310		3320		3330		3340		3350		3360
*	*	*	*	*	*	*	*	*	*	*
TTC	TCT	CAG	GAC	GGT	AAG	GCG	TAC	ACC	CCG	GTC
Phe	Ser	Gln	Asp	Gly	Lys	Ala	Tyr	Thr	Pro	Val

FIG. 1-5

3370	3380	3390	3400	3410	3420
* * *	* * *	* * *	* * *	* * *	* * *
CTC TTT GTG TTC AGC CCA GAC ACA GGT GCT GTC TCT GGC TCC TAC CGA GTT CGA GCC					
Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala					
3430	3440	3450	3460	3470	3480
* * *	* * *	* * *	* * *	* * *	* * *
CTG GAC TAC TGG GCC CGA CCA GGC CCC TTC TCG GAC CCT GTG CCG TAC CTG GAG GTC					
Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val					
3490	3500	3510	3520	3530	3540
* * *	* * *	* * *	* * *	* * *	* * *
CCT GTG CCA AGA GGG CCC CCA TCC CCG GGC AAT CCA TGAG CCTGTGCTGA GCCCCAGTGG					
Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro					
3550	3560	3570	3580	3590	3600
* * *	* * *	* * *	* * *	* * *	* * *
GTTCACCTC CACCGGCAGT CAGCGAGCTG GGGCTGCACT GTGCCCATGC TGCCCTCCCA TCACCCCTT					
3620	3630	3640	3650	3660	3670
* * *	* * *	* * *	* * *	* * *	* * *
TGCAATATAT TTTTATATTT TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA					
3690	3700	3710	3720	3730	3740
* * *	* * *	* * *	* * *	* * *	* * *
AAAAAAAAAA AAAAAAAAAAG AATTCCTGCA GCCCGGGGGA TCCACTAGTT CTAGAGGGCC CGTTTAAACC					
3760	3770	3780	3790	3800	3810
* * *	* * *	* * *	* * *	* * *	* * *
CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCTT					
3830	3840	3850	3860	3870	3880
* * *	* * *	* * *	* * *	* * *	* * *
TGACCCTGGA AGGTGCCACT CCCACTGTCC TTTCCTAATA AAATGAGGAA ATTGCATCGC ATTGTCTGAG					
3900	3910	3920	3930	3940	3950
* * *	* * *	* * *	* * *	* * *	* * *
TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACAATAGC					
3970	3980	3990	4000	4010	4020
* * *	* * *	* * *	* * *	* * *	* * *
AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGGC TCGAGAGCTT					
4040	4050	4060	4070	4080	4090
* * *	* * *	* * *	* * *	* * *	* * *
GGCGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA					
4110	4120	4130	4140	4150	4160
* * *	* * *	* * *	* * *	* * *	* * *
GCCGGAAGCA TAAAGTGTA AGCCTGGGGT GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTGCGCT					
4180	4190	4200	4210	4220	4230
* * *	* * *	* * *	* * *	* * *	* * *
CACTGCCCCG TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG					
4250	4260	4270	4280	4290	4300
* * *	* * *	* * *	* * *	* * *	* * *
AGGCGGTTTG CGTATTGGGC GCTCTCCGC TTCTCGCTC ACTGACTCGC TGCCTCGGT CGTTCGGCTG					
4320	4330	4340	4350	4360	4370
* * *	* * *	* * *	* * *	* * *	* * *
CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA					

FIG. 1-6

4390	4400	4410	4420	4430	4440	4450
* *	* *	* *	* *	* *	* *	* *
AGAACATGTG	AGCAAAAGGC	CAGCAAAAGG	CCAGGAACCG	TAAAAAGGCC	GCGTTGCTGG	CGTTTTTCCA
4460	4470	4480	4490	4500	4510	4520
* *	* *	* *	* *	* *	* *	* *
TAGGCTCCGC	CCCCCTGACG	AGCATCACAA	AAATCGACGC	TCAAGTCAGA	GGTGGCGAAA	CCCGACAGGA
4530	4540	4550	4560	4570	4580	4590
* *	* *	* *	* *	* *	* *	* *
CTATAAAGAT	ACCAGGCGTT	TCCCCCTGGA	AGCTCCCTCG	TGCGCTCTCC	TGTTCCGACC	CTGCCGCTTA
4600	4610	4620	4630	4640	4650	4660
* *	* *	* *	* *	* *	* *	* *
CCGGATACCT	GTCCGCCTTT	CTCCCTTCGG	GAAGCGTGCC	GCTTTCTCAA	TGCTCAGCT	GTAGGTATCT
4670	4680	4690	4700	4710	4720	4730
* *	* *	* *	* *	* *	* *	* *
CAGTTCGGTG	TAGGTCGTT	GCTCCAAGCT	GGGCTGTGTG	CACGAACCCC	CCGTTAGCC	CGACCGCTGC
4740	4750	4760	4770	4780	4790	4800
* *	* *	* *	* *	* *	* *	* *
GCCTTATCCG	GTAAGTATCG	TCTTGAGTCC	AACCCGGTAA	GACACGACTT	ATCGCCACTG	GCAGCAGCCA
4810	4820	4830	4840	4850	4860	4870
* *	* *	* *	* *	* *	* *	* *
CTGGTAACAG	GATTAGCAGA	GCGAGGTATG	TAGGCGGTGC	TACAGAGTTC	TTGAAGTGGT	GGCCTAACTA
4880	4890	4900	4910	4920	4930	4940
* *	* *	* *	* *	* *	* *	* *
CGGCTACACT	AGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT
4950	4960	4970	4980	4990	5000	5010
* *	* *	* *	* *	* *	* *	* *
GGTAGCTCTT	GATCCGGCAA	ACAAACCACC	GCTGGTAGCG	GTGGTTTTTT	TGTTTGCAAG	CAGCAGATTA
5020	5030	5040	5050	5060	5070	5080
* *	* *	* *	* *	* *	* *	* *
CGCGCAGAAA	AAAAGGATCT	CAAGAAGATC	CTTTGATCTT	TTCTACGGGG	TCTGACGCTC	AGTGAACGA
5090	5100	5110	5120	5130	5140	5150
* *	* *	* *	* *	* *	* *	* *
AAACTCACGT	TAAGGGATTT	TGGTCATGAG	ATTATCAAAA	AGGATCTTCA	CCTAGATCCT	TTTAAATTAA
5160	5170	5180	5190	5200	5210	5220
* *	* *	* *	* *	* *	* *	* *
AAATGAAGTT	TTAAATCAAT	CTAAAGTATA	TATGAGTAAA	CTTGGTCTGA	CAGTTACCAA	TGCTTAATCA
5230	5240	5250	5260	5270	5280	5290
* *	* *	* *	* *	* *	* *	* *
GTGAGGCACC	TATCTCAGCG	ATCTGTCTAT	TTCGTTTCATC	CATAGTTGCC	TGACTCCCCG	TCGTGTAGAT
5300	5310	5320	5330	5340	5350	5360
* *	* *	* *	* *	* *	* *	* *
AACTACGATA	CGGGAGGGCT	TACCATCTGG	CCCCAGTGCT	GCAATGATAC	CGCGAGACCC	ACGCTACCCG
5370	5380	5390	5400	5410	5420	5430
* *	* *	* *	* *	* *	* *	* *
GCTCCAGATT	TATCAGCAAT	AAACCAGCCA	GCCGGAAGGG	CCGAGCGCAG	AAGTGGTCCT	GCAACTTTAT
5440	5450	5460	5470	5480	5490	5500
* *	* *	* *	* *	* *	* *	* *
CCGCCTCCAT	CCAGTCTATT	AATTGTTGCC	GGGAAGCTAG	AGTAAGTAGT	TCGCCAGTTA	ATAGTTTGCG

FIG. 1-7

5510	5520	5530	5540	5550	5560	5570
* *	* *	* *	* *	* *	* *	* *
CAACGTTGTT	GCCATTGCTA	CAGGCATCGT	GGTGTACGCG	TCGTCGTTTG	GTATGGCTTC	ATTCAGCTCC
5580	5590	5600	5610	5620	5630	5640
* *	* *	* *	* *	* *	* *	* *
GGTTCCCAAC	GATCAAGGCG	AGTTACATGA	TCCCCATGT	TGTGCAAAAA	AGCGGTTAGC	TCCTTCGGTC
5650	5660	5670	5680	5690	5700	5710
* *	* *	* *	* *	* *	* *	* *
CTCCGATCGT	TGTCAGAAGT	AAGTTGGCCG	CAGTGTATC	ACTCATGGTT	ATGGCAGCAC	TGCATAATTC
5720	5730	5740	5750	5760	5770	5780
* *	* *	* *	* *	* *	* *	* *
TCTTACTGTC	ATGCCATCCG	TAAGATGCTT	TTCTGTGACT	GGTGAGTACT	CAACCAAGTC	ATTCTGAGAA
5790	5800	5810	5820	5830	5840	5850
* *	* *	* *	* *	* *	* *	* *
TAGTGTATGC	GGCGACCGAG	TTGCTCTTGC	CCGGCGTCAA	TACGGGATAA	TACCGCGCCA	CATAGCAGAA
5860	5870	5880	5890	5900	5910	5920
* *	* *	* *	* *	* *	* *	* *
CTTTAAAGT	GCTCATCATT	GGAAAACGTT	CTTCGGGGCG	AAAACTCTCA	AGGATCTTAC	CGCTGTTGAG
5930	5940	5950	5960	5970	5980	5990
* *	* *	* *	* *	* *	* *	* *
ATCCAGTTCG	ATGTAACCCA	CTCGTGCACC	CAACTGATCT	TCAGCATCTT	TTACTTTTAC	CAGCGTTTCT
6000	6010	6020	6030	6040	6050	6060
* *	* *	* *	* *	* *	* *	* *
GGGTGAGCAA	AAACAGGAAG	GCAAAATGCC	GCAAAAAAGG	GAATAAGGGC	GACACGGAAA	TGTTGAATAC
6070	6080	6090	6100	6110	6120	6130
* *	* *	* *	* *	* *	* *	* *
TCATACTCTT	CCTTTTTCAA	TATTATTGAA	GCATTTATCA	GGGTTATTGT	CTCATGAGCG	GATACATATT
6140	6150	6160	6170	6180	6190	6200
* *	* *	* *	* *	* *	* *	* *
TGAATGTATT	TAGAAAAATA	AACAAATAGG	GGTCCGCGC	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC

Fig. 2A

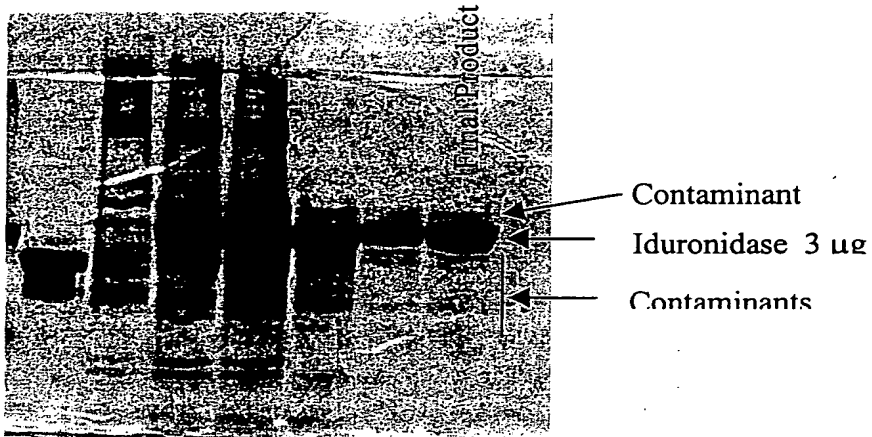
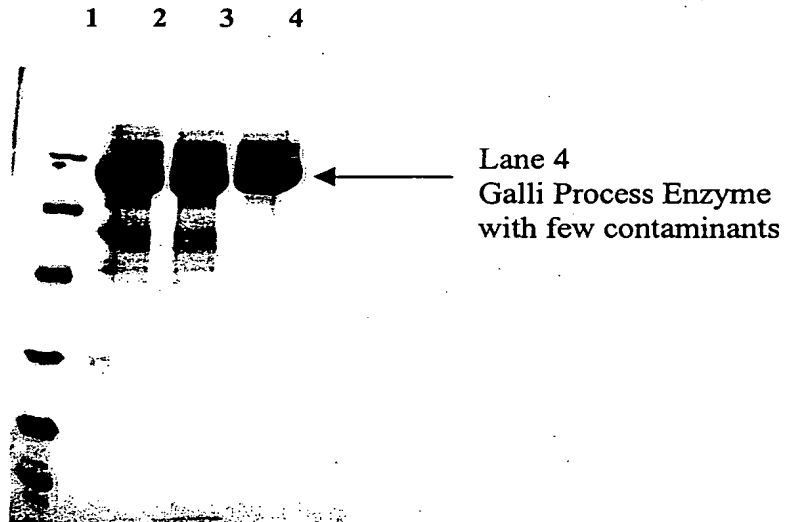


Fig. 2B



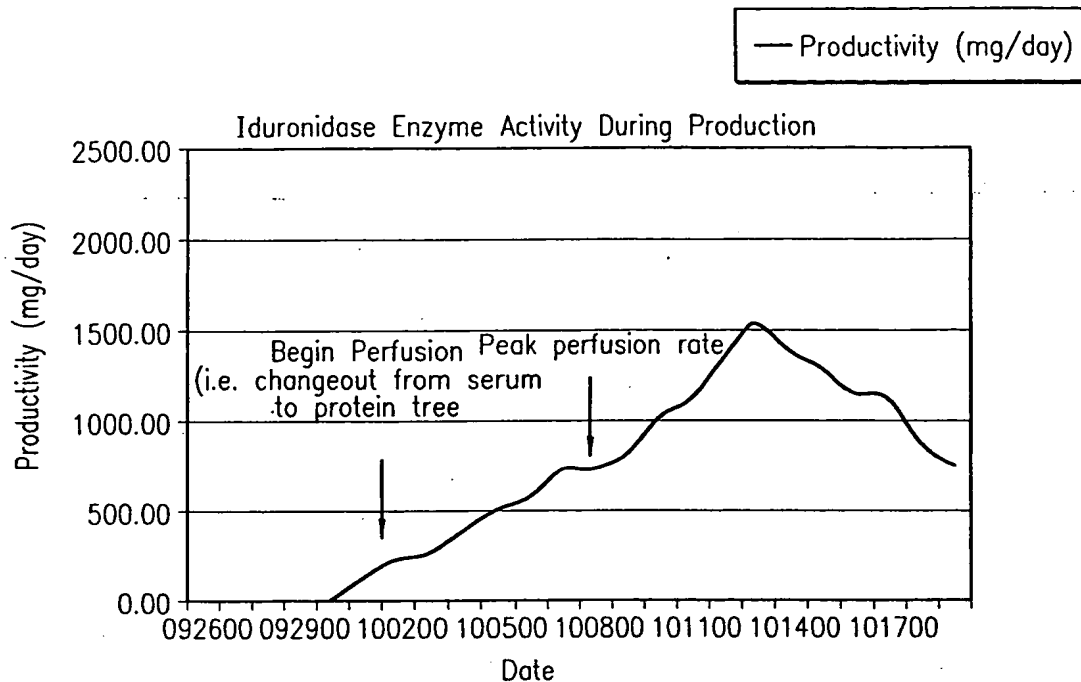


FIG. 3A

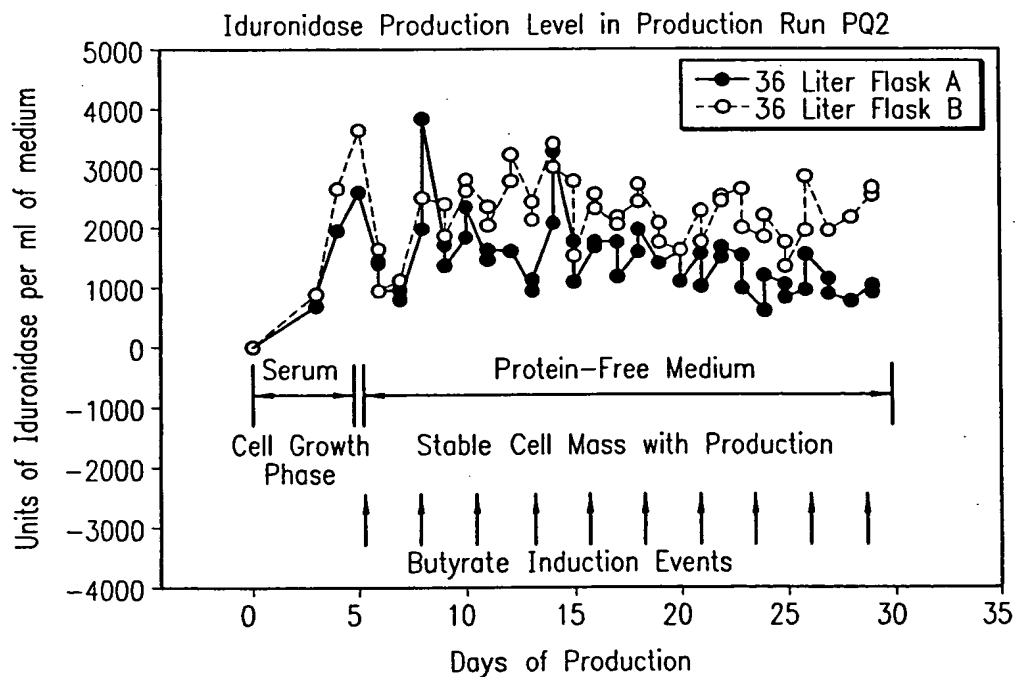
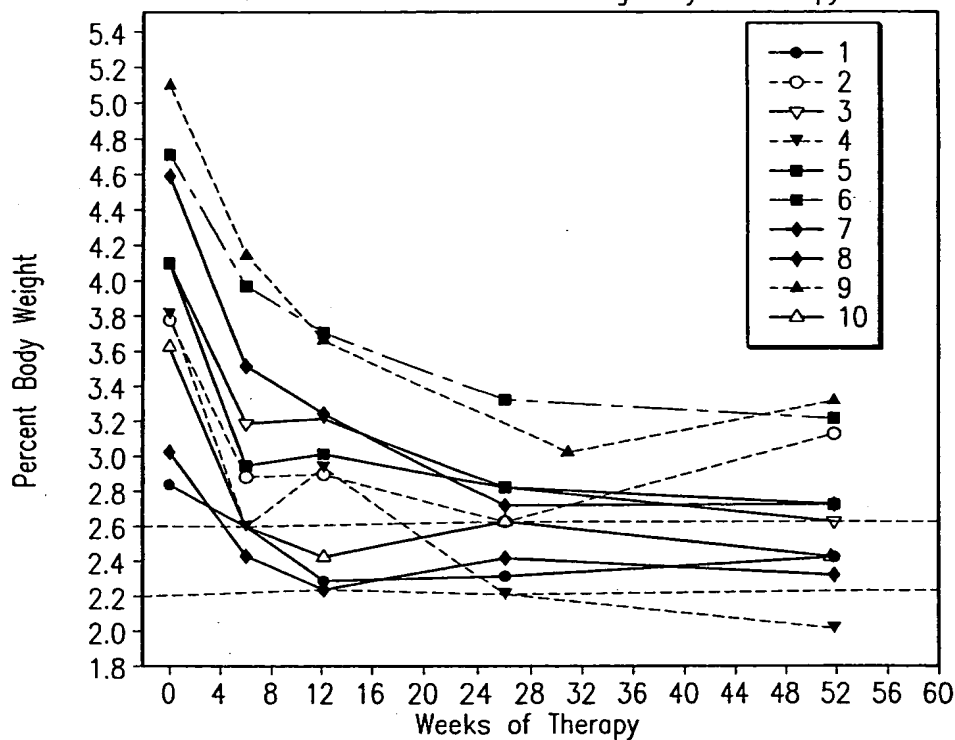


FIG. 3B

FIG. 4

Reduction in Liver Volume During Enzyme Therapy



Urinary GAG Excretion During Enzyme Therapy

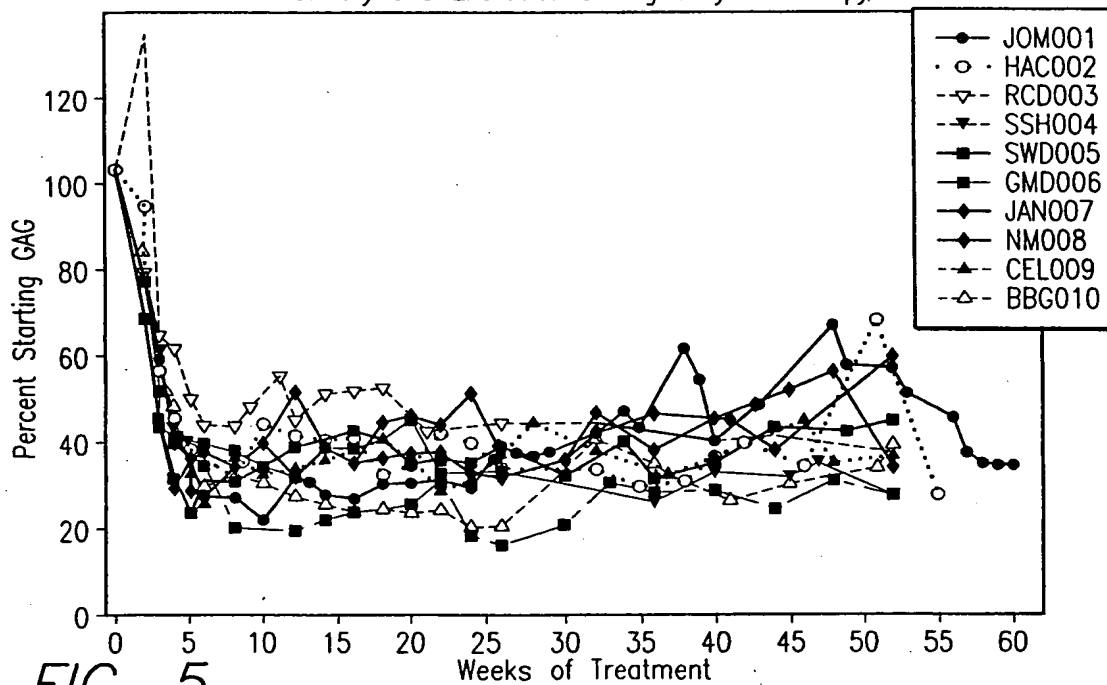
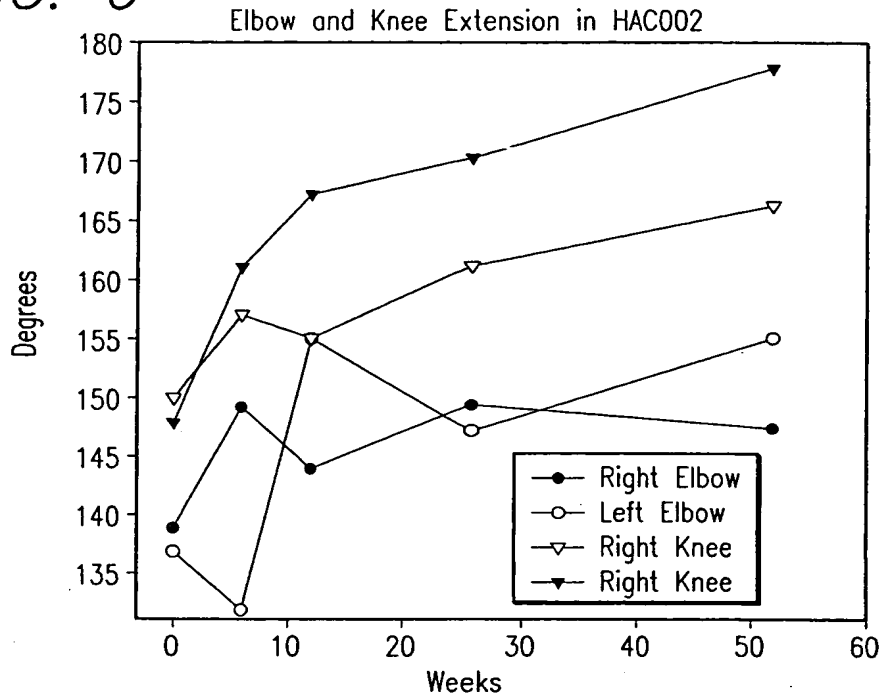
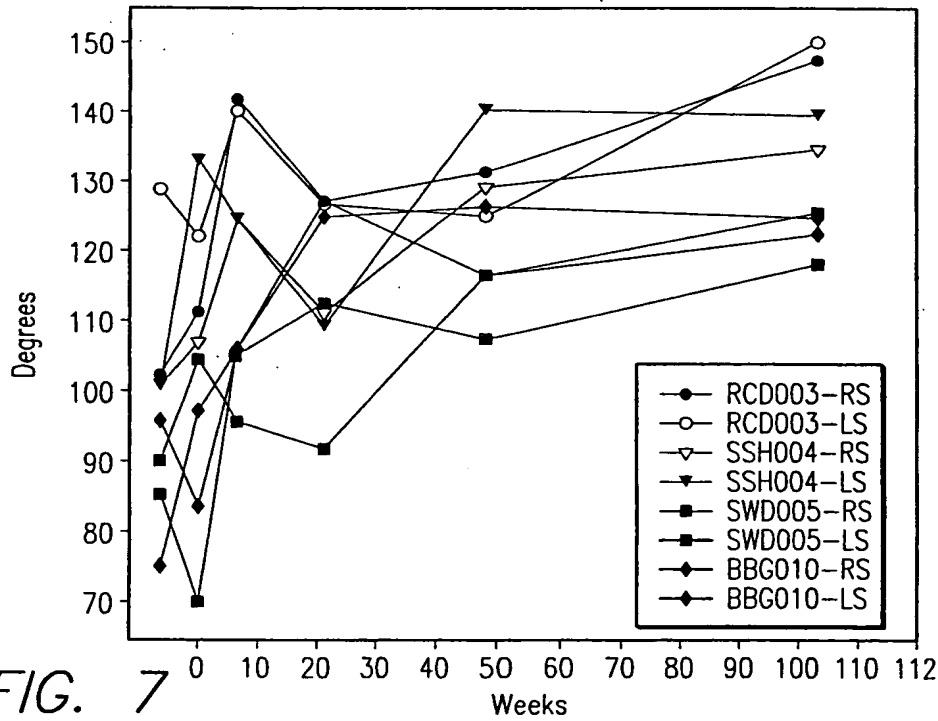


FIG. 5

FIG. 6



Shoulder flexion to 104 weeks in four patients with most restriction



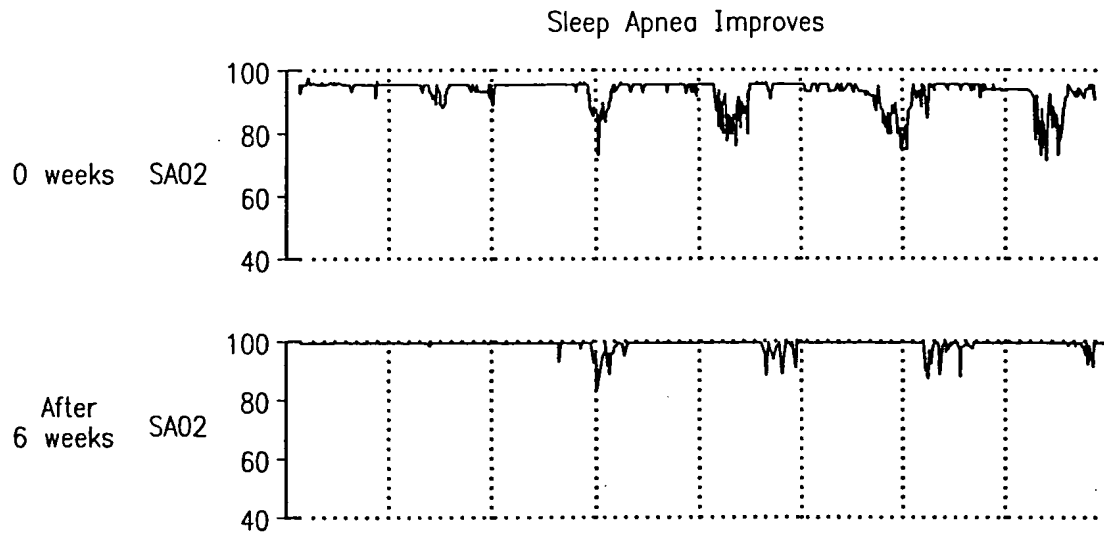


FIG. 8

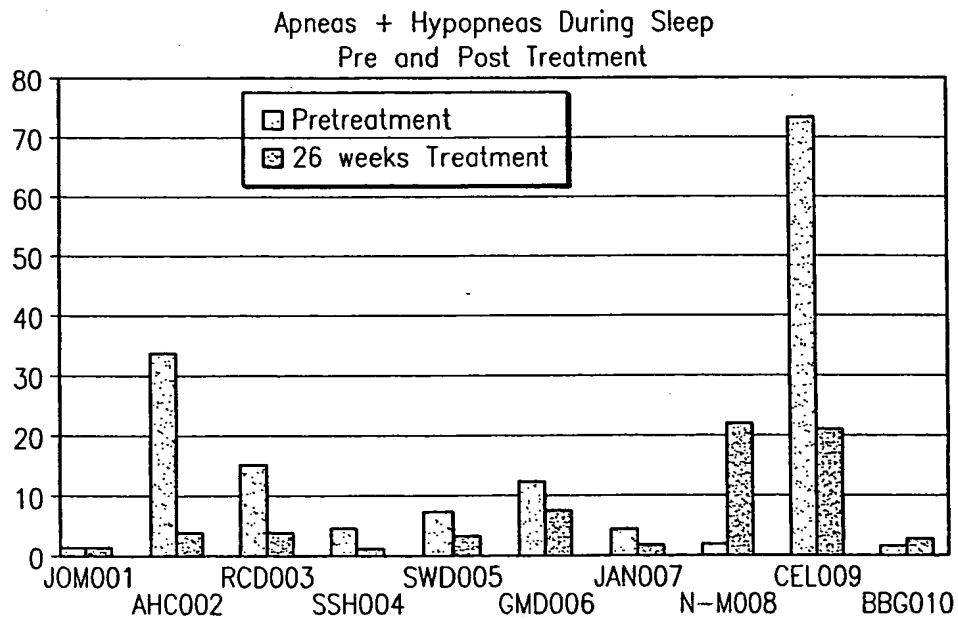


FIG. 9

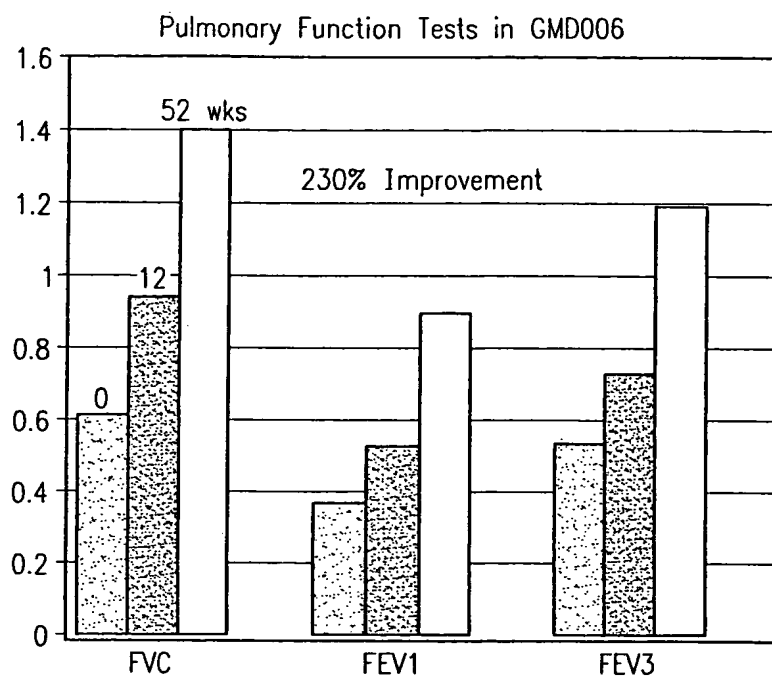


FIG. 10

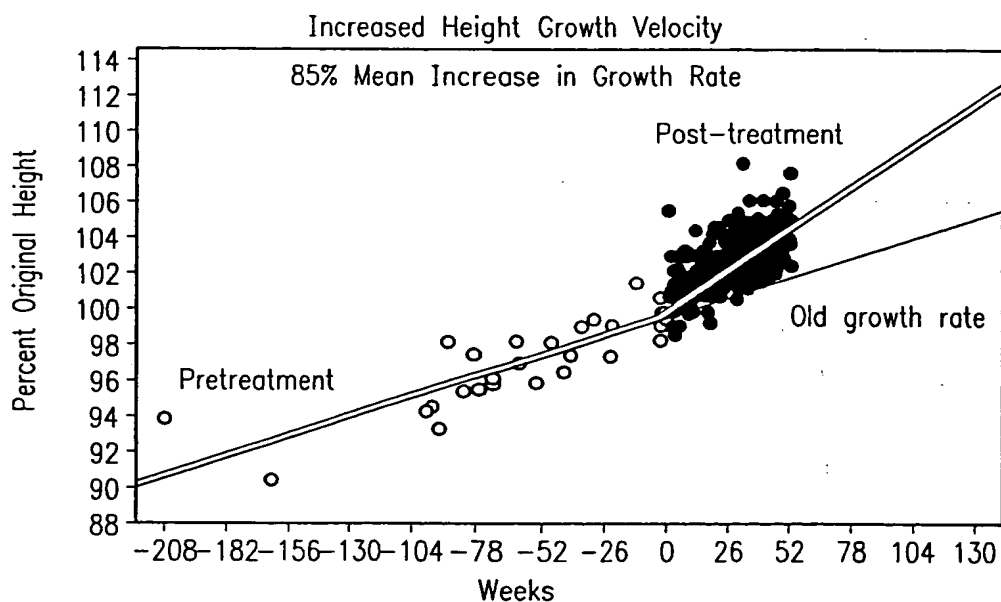


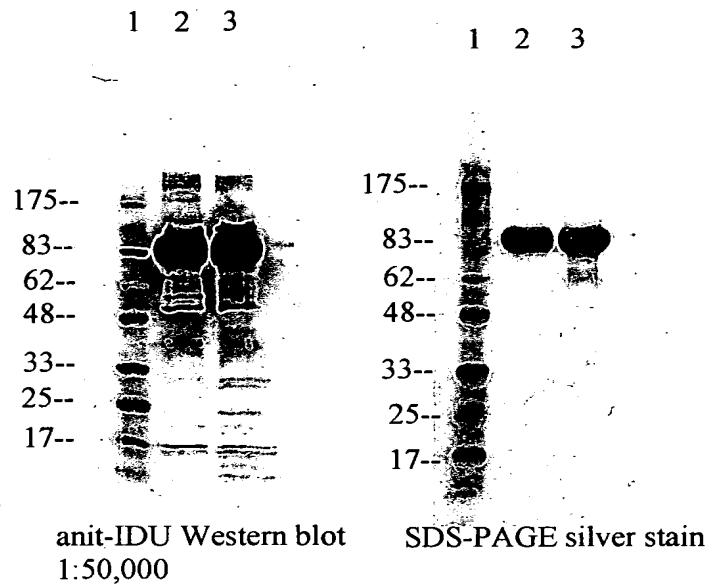
FIG. 11

FIG. 12

Chinese Hamster Ovary Host Protein Contamination by ELISA Assay

SOURCE AND BATCH NUMBER	CHOP PROTEIN CONTAMINATION (microgram per milligram)	PERCENT CHOP CONTAMINATION	PURITY OF THE ENZYME FROM CHOP
Prior Process (Carson/REI)			
C9002	14	1.4%	98.6%
C9003	24	2.4%	97.6%
C9004	16	1.6%	98.4%
New Process (Galli)			
P1003	<1.3	<0.13%	>99.9%
P1006	1.2	0.12%	99.9%
P1007	<0.6	<0.06%	>99.9%
P1008	<0.67	<0.067%	>99.9%

Comparison of Galli and Carson Material



- 1 Marker
- 2 Galli Referenced-0201
- 3 Carson C9002

5ug/lane

FIG. 13